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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2010; month=2; day=5; hr=8; min=56; sec=2; ms=894; ]

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Application No: 10574084

Version No: 2.0

Input Set:

Output Set:

Started: 2010-01-25 15:31:31.523

Finished: 2010-01-25 15:31:34.844

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 321 ms

Total Warnings: 44

Total Errors: 0

No. of SeqIDs Defined: 46

Actual SeqID Count: 46

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W 213	Artificial or Unknown found in <213> in SEQ ID (19)
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**Input Set:**

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Error code

Error Description

This error has occurred more than 20 times, will not be displayed

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<120> AA method of modulating cell survival, differentiation and/or synaptic plasticity

<130> P 810 PC00

<140> 10574084

<141> 2010-01-25

<160> 46

<170> PatentIn version 3.5

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<212> PRT

<213> Artificial sequence

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Asp Val Arg  
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Gln Glu Phe Lys Glu Gly Glu Asp Ala Val Ile Val  
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<220>

<223> rat NCAM Ig2 fragment: amino acid residues 111-121

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<223> rat NCAM Ig1 fragment: amino acid residues 10-21

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Gly Glu Ile Ser Val Gly Glu Ser Lys Phe Phe Leu  
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<211> 21

<212> PRT



<213> Artificial sequence

<220>

<223> rat NCAM Ig3 fragment: amino acid residues 243-263

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Asp Lys Asn Asp Glu  
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<210> 21

<211> 12

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<220>

<223> rat NCAM Ig1 fragment : amino acid residues 10-21 containing  
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<210> 22

<211> 12

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mutations F19A and F20A

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<210> 23

<211> 21

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<220>

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Asp Lys Ser Asp Glu  
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<210> 24  
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Lys Tyr Ser Phe Asn Tyr Asp Gly Ser Glu  
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<220>  
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mutations K285A and F287S  
  
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Ser Ile His Leu Ala Val Ala Ala Lys  
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<400> 27

Ser Ile His Leu Ala Val Gly Ala Lys  
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<210> 28

<211> 12

<212> PRT

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<223> rat NCAM Ig2 fragment: amino acid residues 172-182

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aaaccgggt tactttgcaa agacctt

27

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<211> 25

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<220>  
<223> NCAM Ig1 fragment: FG-strands

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<210> 42  
<211> 10  
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<220>  
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Asp Val Arg Arg Gly Ile Lys Lys Thr Asp  
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<210> 43  
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<220>  
<223> NCAM Ig2 fragment: EF-strands

<400> 43

Gln Ile Arg Gly Ile Lys Lys Thr Asp  
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<210> 44  
<211> 858  
<212> PRT  
<213> Rattus norvegicus

<400> 44

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20 25 30

Val Gly Glu Ser Lys Phe Phe Leu Cys Gln Val Ala Gly Asp Ala Lys  
35 40 45

Asp Lys Asp Ile Ser Trp Phe Ser Pro Asn Gly Glu Lys Leu Ser Pro  
50 55 60

Asn Gln Gln Arg Ile Ser Val Val Trp Asn Asp Asp Asp Ser Ser Thr  
65 70 75 80

Leu Thr Ile Tyr Asn Ala Asn Ile Asp Asp Ala Gly Ile Tyr Lys Cys  
85 90 95

Val Val Thr Ala Glu Asp Gly Thr Gln Ser Glu Ala Thr Val Asn Val  
100 105 110

Lys Ile Phe Gln Lys Leu Met Phe Lys Asn Ala Pro Thr Pro Gln Glu  
115 120 125

Phe Lys Glu Gly Glu Asp Ala Val Ile Val Cys Asp Val Val Ser Ser  
130 135 140

Leu Pro Pro Thr Ile Ile Trp Lys His Lys Gly Arg Asp Val Ile Leu  
145 150 155 160

Lys Lys Asp Val Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile  
165 170 175

Arg Gly Ile Lys Lys Thr Asp Glu Gly Thr Tyr Arg Cys Glu Gly Arg  
180 185 190

Ile Leu Ala Arg Gly Glu Ile Asn Phe Lys Asp Ile Gln Val Ile Val  
195 200 205

Asn Val Pro Pro Thr Val Gln Ala Arg Gln Ser Ile Val Asn Ala Thr  
210 215 220

Ala Asn Leu Gly Gln Ser Val Thr Leu Val Cys Asp Ala Asp Gly Phe  
225 230 235 240

Pro Glu Pro Thr Met Ser Trp Thr Lys Asp Gly Glu Pro Ile Glu Asn  
245 250 255

Glu Glu Glu Asp Asp Glu Lys His Ile Phe Ser Asp Asp Ser Ser Glu

260

265

270

Leu Thr Ile Arg Asn Val Asp Lys Asn Asp Glu Ala Glu Tyr Val Cys  
 275 280 285

Ile Ala Glu Asn Lys Ala Gly Glu Gln Asp Ala Ser Ile His Leu Lys  
 290 295 300

Val Phe Ala Lys Pro Lys Ile Thr Tyr Val Glu Asn Gln Thr Ala Met  
 305 310 315 320

Glu Leu Glu Glu Gln Val Thr Leu Thr Cys Glu Ala Ser Gly Asp Pro  
 325 330 335

Ile Pro Ser Ile Thr Trp Arg Thr Ser Thr Arg Asn Ile Ser Ser Glu  
 340 345 350

Glu Lys Ala Ser Trp Thr Arg Pro Glu Lys Gln Glu Thr Leu Asp Gly  
 355 360 365

His Met Val Val Arg Ser His Ala Arg Val Ser Ser Leu Thr Leu Lys  
 370 375 380

Ser Ile Gln Tyr Thr Asp Ala Gly Glu Tyr Ile Cys Thr Ala Ser Asn  
 385 390 395 400

Thr Ile Gly Gln Asp Ser Gln Ser Met Tyr Leu Glu Val Gln Tyr Ala  
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Pro Lys Leu Gln Gly Pro Val Ala Val Tyr Thr Trp Glu Gly Asn Gln  
 420 425 430

Val Asn Ile Thr Cys Glu Val Phe Ala Tyr Pro Ser Ala Thr Ile Ser  
 435 440 445

Trp Phe Arg Asp Gly Gln Leu Leu Pro Ser Ser Asn Tyr Ser Asn Ile  
 450 455 460

Lys Ile Tyr Asn Thr Pro Ser Ala Ser Tyr Leu Glu Val Thr Pro Asp  
 465 470 475 480

Ser Glu Asn Asp Phe Gly Asn Tyr Asn Cys Thr Ala Val Asn Arg Ile  
 485 490 495



Gly Gln Glu Ser Leu Glu Phe Ile Leu Val Gln Ala Asp Thr Pro Ser  
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Ser Pro Ser Ile Asp Arg Val Glu Pro Tyr Ser Ser Thr Ala Gln Val  
515 520 525

Gln Phe Asp Glu Pro Glu Ala Thr Gly Gly Val Pro Ile Leu Lys Tyr  
530 535 540

Lys Ala Glu Trp Lys Ser Leu Gly Glu Glu Ala Trp His Ser Lys Trp  
545 550 555 560

Tyr Asp Ala Lys Glu Ala Asn Met Glu Gly Ile Val Thr Ile Met Gly  
565 570 575

Leu Lys Pro Glu Thr Arg Tyr Ala Val Arg Leu Ala Ala Leu Asn Gly  
580 585 590

Lys Gly Leu Gly Glu Ile Ser Ala Ala Thr Glu Phe Lys Thr Gln Pro  
595 600 605

Val Arg Glu Pro Ser Ala Pro Lys Leu Glu Gly Gln Met Gly Glu Asp  
610 615 620

Gly Asn Ser Ile Lys Val Asn Leu Ile Lys Gln Asp Asp Gly Gly Ser  
625 630 635 640

Pro Ile Arg His Tyr Leu Val Lys Tyr Arg Ala Leu Ala Ser Glu Trp  
645 650 655

Lys Pro Glu Ile Arg Leu Pro Ser Gly Ser Asp His Val Met Leu Lys  
660 665 670

Ser Leu Asp Trp Asn Ala Glu Tyr Glu Val Tyr Val Val Ala Glu Asn  
675 680 685

Gln Gln Gly Lys Ser Lys Ala Ala His Phe Val Phe Arg Thr Ser Ala  
690 695 700

Gln Pro Thr Ala Ile Pro Ala Asn Gly Ser Pro Thr Ala Gly Leu Ser  
705 710 715 720

Thr Gly Ala Ile Val Gly Ile Leu Ile Val Ile Phe Val Leu Leu Leu  
725 730 735

Val Val Met Asp Ile Thr Cys Tyr Phe Leu Asn Lys Cys Gly Leu Leu  
740 745 750

Met Cys Ile Ala Val Asn Leu Cys Gly Lys Ala Gly Pro Gly Ala Lys  
755 760 765

Gly Lys Asp Met Glu Glu Gly Lys Ala Ala Phe Ser Lys Asp Glu Ser  
770 775 780

Lys Glu Pro Ile Val Glu Val Arg Thr Glu Glu Glu Arg Thr Pro Asn  
785 790 795 800

His Asp Gly Gly Lys His Thr Glu Pro Asn Glu Thr Thr Pro Leu Thr  
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Glu Pro Glu Lys Gly Pro Val Glu Thr Lys Ser Glu Pro Gln Glu Ser  
820 825 830

Glu Ala Lys Pro Ala Pro Thr Glu Val Lys Thr Val Pro Asn Glu Ala  
835 840 845

Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala  
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